AMENDMENTS

In the claims:

Please cancel claims 39-71 without prejudice or disclaimer, and please amend claim 34, as set forth in the following complete listing of the claims, which replaces all other listings of the claims.

1 (Original). A method for identifying a subject at risk of osteoarthritis, which comprises detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the one or more polymorphic variations are detected in a nucleotide sequence in SEQ ID NO: 1-13, or referenced in Table B, or a substantially identical sequence thereof, or a fragment of the foregoing; whereby the presence of the polymorphic variation is indicative of the subject being at risk of osteoarthritis.

2 (Original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 21233000 to 21243000 of chromosome 2 in human genomic DNA.

4 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 238, 294, 295, 347, 1425, 4891, 5087, 7041, 7121, 7219, 7443, 7485, 10939, 11367, 11571, 11839, 12551, 12646, 13469, 14913, 15205, 15246, 15695, 17473, 17610, 17828, 18130, 18281, 18623, 18890, 21561, 23100, 23872, 24581, 24582, 24983, 27540, 30846, 31415, 31453, 31899, 37000, 38681, 39287, 42951, 45648, 46222, 46687, 47020, 47593, 48513, 49723, 49986, 53018, 53296, 53547, 53899, 53916, 53933, 54305, 55327, 55895, 56143, 56640, 58486, 59576, 63048, 64008, 64018, 64859, 65995, 66905, 67183, 67942, 68101, 68521, 68664, 68988, 69178, 72143, 74183, 74312, 74407, 75518, 76153, 77398, 77615, 79092, 80000, 80125, 80595, 81061, 81151, 81918, 83072, 83137, 83235, 83263, 83279, 83280, 83533, 86856, 87186, 87189, 87727, 87978, 89129, 89556, 89702, 90233, 93060, 94779, 95367, 95844, 95942, 96884 , 96938, 97627, 97777, 97871, 98746 and 99663.

5 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 7219, 7485, 11839, 31899, 37000, 48513, 49986, 56640, 74407, 77398, 93060 and 97627.

6 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 102456500 to 102471500 of chromosome 2 in human genomic DNA.

7 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 225, 509, 860, 874, 939, 1483, 1798, 2189, 2215, 2282, 2340, 2963, 3369, 3481, 3564, 3653, 4860, 4941, 4975, 5321, 5346, 5541, 5633, 6007, 6317, 6378, 6382, 6426, 6479, 6641, 6703, 6705, 7963, 8525, 8526, 8598, 8624, 8883, 8980, 13578, 16135, 16141, 16642, 16931, 17004, 17009, 17010, 18713, 18853, 20783, 21335, 22180, 22268, 22285, 25378, 25906, 26015, 26475, 26798, 27042, 27649, 27827, 27873, 28122, 28202, 28232, 28240, 29546, 29748, 30054, 30646, 31149, 36912, 36936, 37184, 39064, 39343, 40868, 40917, 41113, 47343, 47806, 47911, 48009, 48621, 49245, 49247, 49299, 49302, 49514, 49626, 49791, 50010, 50294, 51482, 51556, 51855, 51956 ,52155, 52448, 52458, 52511, 52607, 54049, 54224, 54567, 55052, 55857, 55941, 56120, 56349, 56727, 57232, 58806, 61181, 63808, 64526, 64865, 64928, 64966, 65080, 65690, 66228, 66982, 72511, 74170, 74264, 74333, 74502, 74741, 75321, 82558, 85366, 85469, 86485, 87687, 89463, 89660, 95718 and 95821.

8 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 2215, 3369, 16642, 20783, 52155, 55052, 55941, 74333, 74741, 85366, 85469, 87687, 89660 and 95718.

9 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 102570000 to 102583000 of chromosome 2 in human genomic DNA.

10 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 207,

6019, 6414, 7341, 10984, 12351, 13335, 16584, 16737, 23897, 24057, 25145, 25300, 26262, 26312, 26589, 27302, 27358, 27451, 27552, 30731, 32085, 32139, 33184, 42382, 42569, 44823, 45217, 45548, 45601, 45722, 45967 ,47367, 47642, 48126, 49218, 49274, 49433, 49610, 51282, 51466, 53757, 53960, 54031, 54574, 55679, 56100, 56182, 59817, 60533, 60656, 72209, 72778, 74293, 77335, 78029, 78374, 78421, 78434, 79174, 79397, 79562, 79700, 79730, 79904, 79920, 79938, 79972, 80125, 80368, 83484, 85536, 85829, 86425, 88083, 88770, 90622, 90924, 91634, 92029, 95152, 95348, 96145, 96793, 97015, 97064, 97711, 97855 and 98708.

11 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 6414, 51282, 54574, 78374, 92029 and 96793.

12 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions positions 175647734 to 175655734 of chromosome 2 in human genomic DNA.

13 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 209, 5908, 7460, 7733, 7855, 7904, 8869, 9480, 13820, 15152, 17713, 17804, 18220, 19083, 19123, 19605, 20247, 20592, 21907, 23273, 23299, 23623, 23669, 23844, 24190, 24486, 24896, 25118, 30551, 30844, 30900, 30942, 31699, 32081, 35078, 36196, 36541, 38356, 45578, 49634, 49774, 51119, 51181, 51652, 54467, 55762, 55999, 57865, 66613, 68377, 69754, 72859, 76512, 76717, 77722, 80998, 82033, 89658, 89960, 94155 and 95679.

14 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 19083, 30900, 38356, 76512 and 94155.

15 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 178746000 to 178751000 of chromosome 5 in human genomic DNA.

16 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 6 selected from the group consisting of 210, 3608, 3609, 4318, 5593, 5629, 5639, 5640, 8943, 17968, 19887, 21034, 21085, , 21596, 23379, 23432, 24007, 26121, 26273, 26755, 27411, 27710, 27842, 28379, 29603, 31232, 31504, 32583, 32794, 32840, 33044, 33150, 33218, 33513, 33959, 34486, 36289, 36570, 38247, 38477, 38518, 38529, 38667, 39781, 39856, 39927, 40506, 41869, 42452, 44788, 46059, 46846, 47712, 48796, 49441, 49602, 49723, 50050, 50171, 50477, 50818, 50833, 50881, 50882, 51386, 51534, 52317, 52368, 52970, 53023, 53356, 53882, 54553, 55475, 55530, 55691, 55848, 55879, 56316, 56911, 57320, 57391, 57437, 57478, 57500, 59111, 59333, 59715, 59804, 59851, 59929, 60052, 60240, 60359, 60381, 60456, 60724, 60875, 60968, 60978, 60998, 61557, 62091, 62645, 62943, 63131, 63145, 63406, 63427, 63554, 63661, 64093, 64153, 64409, 64544, 65257, 65626,65739 , 66392, 66720, 69177, 69336, 69636, 69823, 69928, 70547, 70633, 71805, 72181, 72200, 72474, 72567, 72973, 73468, 73889, 75730, 75970, 76114, 76342, 76449, 76465, 76791, 78042, 80758, 80778, 81356, 81576, 81689, 81759, 81950, 82562, 83591, 83700, 83821, 83842, 83923, 83929, 84021, 84175, 84417, 84747, 85746, 86129, 86335, 87315, 87648, 87764, 87770, 88221, 90474, 91148, 91150, 91160, 91733, 91772, 91785, 93140, 93148, 96080, 96157, 96313, 96759, 97026, 97320, 97732, 98713, 99707, 99959, 100009, 100020, 100065, 100086, 101270, 101276, 101371, 101376, 101439, 101820, 102392, 102602, 102604, 102896, 189104, 189134 and 189205.

17 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 6 selected from the group consisting of 5640, 33150, 38247, 38529, 46846, 49723, 50050, 63427, 73889, 189104 and rs428901.

18 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 105595000 to 105615000 of chromosome 6 in human genomic DNA.

19 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 7 selected from the group consisting of 241, 801, 899, 2091, 2290, 2440, 4959, 7914, 7969, 7972, 10831, 12399, 13841, 14461, 14680, 16808, 18231, 18394, 18505, 18684, 19257, 20263, 20656, 21499, 21563, 21612, 21834, 22406, 22408, 22685, 23303, 23306, 25139, 25211, 25364, 25381, 25414, 25835, 26214, 27224, 27526, 27934, 28550, 29015, 29879, 29979, 30030, 30585, 31753, 31934, 33227, 33228, 35172, 36901, 36921,

36932, 37061, 37570, 38745, 38970, 39725, 40070, 40460, 41470, 41562, 41956, 42047, 42280, 42358, 42629, 43075, 43387, 43393, 43438, 44115, 44537, 45642, 46629,47496, 47515, 48329, 48862, 48908, 49038, 49080, 50204, 50404, 50426, 50531, 50840, 50964, 50971,51378, 52610, 53906, 53951, 54111, 54149, 55563, 55999, 58415, 58961, 60447, 61377, 61528, 61606, 62140, 62461, 63826, 64950, 65076, 66121, 66406, 67051, 68860, 69014, 70796, 72325, 73414, 75258, 76347, 76839, 77358, 77822, 77946, 80002, 80024, 80285, 80397, 82075, 82153, 83981, 84184, 85089, 85288, 85330, 85581, 85642, 86433, 86904, 88391, 89042, 90828, 92676, 92881, 94227, 94585, 94616, 94712, 94738, 95253, 95522, 95869 and 97856.

20 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 7 selected from the group consisting of 25414, 25835, 38970, 41470, 44115, 47496, 49038, 50204, 50840, 50964, 50971, 53906, 54149, 58415, 70796, 72325, 75258, 77822, 80002, 85288, 85581, 86904, 90828, 94616, 94712, 95869 and 97856.

21 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 27052000 to 27066000 of chromosome 12 in human genomic DNA.

22 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 8 selected from the group consisting of 230, 231, 5330, 6334, 11372, 11456, 11501, 13393, 16666, 17596, 19710, 19800, 20297, 20967, 32514, 33159, 37600, 41259, 41329, 50060, 53292, 53393, 56417, 56435, 58847, 59595, 59661, 60355, 60407, 62357, 68230, 68516, 69055, 72603, 73928, 85897 and 91554.

23 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 8 selected from the group consisting of 56435, 59595, 53292, 33159 and 41329.

24 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 71957600 to 71962600 of chromosome 15 in human genomic DNA.

25 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 10 selected from the group consisting of 213, 249, 1824, 2057, 2306, 2869, 3976, 4288, 4290, 4434, 5298, 5467, 8486, 8487, 8831, 9036, 9058, 9131, 9732, 9862, 10191, 10270, 16167, 17620, 17751, 17764, 17787, 19401, 21021, 21902, 22173, 22416, 22653, 24945, 25011, 28563, 48574, 48710, 48880, 50194, 56343, 56455, 56729, 56759, 56895, 57036, 57702, 62515, 62629, 63501, 63547, 64876, 65073, 67149, 67549, 71660, 71906 and 71911.

26 (Original). The method of claim 1, wherein a polymorphic variation is detected at position 65073 in SEQ ID NO: 10.

27 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 76221000 to 76226000 of chromosome 16 in human genomic DNA.

28 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 11 selected from the group consisting of 205, 866, 4212, 5934, 11486, 16969, 22509, 22796, 28097, 28626, 28853, 28873, 30155, 30827, 31956, 32404, 32944, 35205, 35227, 35781, 41052, 45051, 46039, 47276, 47678, 47716, 51014, 54408, 54596, 56853, 61851, 62016, 62461, 68257, 69793, 73976, 73999, 74053, 75315, 75729, 76466, 77216, 77217, 79239, 80825, 81060, 81097, 81426, 84787, 84896, 85165, 86502, 86753, 86941, 88787 and 95598.

29 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 11 selected from the group consisting of 47716 and 69793.

30 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 34828750 and 34833750 of chromosome 22 in human genomic DNA.

31 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 13 selected from the group consisting of

201, 425, 1095, 2201, 7879, 8395, 8461, 9503, 10304, 10695, 16300, 16444, 17591, 17988, 19116, 19358, 20300, 20669, 20891, 21451, 21978, 22785, 24248, 24770, 24844, 25066, 25096, 25309, 25344, 25529, 25537, 25554, 27963, 28134, 28356, 29648, 29986, 30217, 30267, 30315, 30585, 30724, 30897, 30931, 31080, 31246, 31373, 31463, 31467, 32188, 32288, 32520, 32594, 32657, 32677, 32764, 32784, 32830, 32872, 33121, 33348, 33952, 34184, 34361, 35026, 35192, 35600, 36033, 36289, 38869, 39629, 40530, 41621, 42379, 42802, 42865, 43644, 45051, 45828, 45829, 46257, 47286, 47427, 47963, 48013, 48229, 48282, 48376, 48404, 49900, 52699, 52897, 53414, 53487, 54112, 55492, 59766, 60307, 60701, 60952, 61401, 62379, 62870, 62879, 63499, 64284, 64408, 64760, 65230, 66127, , 6634, 66686, 66694, 67113, 67257, 67403, 67609, 68418, 68610, 69629, 70024, 70848, 71428, 71553, 71633, 71768 ,71769, 73039, 73325, 73412, 73547, 73769, 73806, 74467, 74472, 74473, 74482, 74494, 74592, 74670, 74672, 74714, 74723, 74749, 74861, 74892, 74893, 75176, 75705, 75989, 76027, 77949, 77974, 78167, 78310, 78415, 78575, 78590, 78709, 78875, 79864, 81316, 81320, 81409, 81737, 81843, 82102, 82833, 83461, 83624, 83660, 83701, 83708, 83782, 85707, 85717, 86486, 86833, 87115, 87234, 87479, 87561, 87604, 87674, 87958, 87992, 88019, 88074, 88079, 88115, 88118, 88120, 88135, 88142, 88143, 88149, 88340, 88344, 88512, 88521, 88650, 88827, 89230, 89236, 90754, 90984, 91110, 92026, 92954, 93375, 93794, 94937, 95068, 96188, 97092 and 98812.

32 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 13 selected from the group consisting of 20300, 87958, 89236, 30267, 32657, 36289, 38869, 45051, 46257, 54112, 60307, 63499, 20891, 52699 and 71768.

33 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in Table B.

34 (Currently Amended). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in claim 4~~, 7, 10, 13, 16, 19, 22, 25, 28, 31 or 33~~.

35 (Original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

36 (Original). The method of claim 1, wherein the subject is a human.

37 (Original). The method of claim 36, wherein the subject is a human female.

38 (Original). The method of claim 36, wherein the subject is a human male.

39-71 (Cancelled).